What is claimed is:

1. A method if associating a phenotype with the occurrence of a particular set of allelic markers that occur at a plurality of genetic loci in a population of individuals, the method comprising:

a) identifying a phenotype that is expressed by a trait that is quantitatively evaluated on a numeric scale;

b) identifying for each genetic locus of a plurality of genetic loci the form of the allelic marker occurring at a plurality of genetic loci, where said genetic locus is characterized by having at least two allelic forms of a marker and wherein the phenotype is expressed by a trait that is quantitatively evaluated on a numeric scale;

c) identifying a set of said allelic markers present in the nucleic acid of each individual of the population;

d) obtaining the numeric value corresponding to the phenotypic trait for each individual of the population; and

e) obtaining a p-value based on a particular set of markers and the numeric value, wherein the p-value provides the probability that the association of the phenotype with the particular set is due to a random association, whereby obtaining a p-value less than a predetermined limit establishes the association of said phenotype with occurrence of a particular set of a the particular set of allelic markers that occur at a the plurality of genetic loci in a the population of individuals.

2. The method of claim 1, wherein the number of genetic loci is 2, 3, 4, or 5.

3. The method of claim 1, wherein the number of individuals is 5,000 or fewer.

4. The method of claim 1, wherein the number of individuals is 1,000 or fewer.

5. The method of claim 1, wherein the number of individuals is 500 or fewer.

6. The method of claim 1, wherein the number of individuals is 200 or fewer.

7. The method of claim 1, wherein at least one allelic marker is a single nucleotide polymorphism (SNP).

8. The method of claim 1, wherein a genetic locus is characterized by having two allelic forms of the marker.

9. The method of claim 1, wherein at least two genetic loci are in linkage disequilibrium with respect to each other.

10. The method of claim 1, wherein a particular set of allelic markers comprise a haplotype.

11. The method of claim 1, wherein at least two genetic loci comprise a set of super-SNPs.

12. The method of claim 1, wherein the p-value is obtained using a regression analysis.

13. The method of claim 1, wherein the p-value is obtained using analysis of variance.

14. The method of claim 1, wherein the p-value is less than 0.1.

15. The method of claim 1, wherein the p-value is less than 0.03.

16. The method of claim 1, wherein the p-value is less than 0.01.

17. A method of estimating the number of individual samples required to establish the association of a phenotype with occurrence of a particular set of allelic markers that occur at a plurality of genetic loci in a population of individuals, wherein each genetic locus is characterized by having at least two allelic forms of a marker and as being the locus of a set of single nucleotide polymorphisms (SNPs), and wherein the phenotype is expressed by a trait that is quantitatively evaluated on a numeric scale, the method comprising the steps of:

a) determining the number of SNPs to be evaluated;

b) combining consecutive SNPs that are in linkage disequilibrium into super-SNPs;

c) determining the number of haplotypes; and

d) determining the estimated number of samples required.

18. The method of claim 17, wherein the number of SNPs plus the number of super-SNPs is smaller than the number of haplotypes, and wherein the estimating uses the formula provided on the last line of Table 1 in column 2 or column 3.

19. The method of claim 17, wherein the number of SNPs plus the number of super-SNPs is greater than the number of haplotypes, and wherein the estimating uses the formula provided on the last line of Table 1 in column 4.

20. The method of claim 17, wherein the number of haplotypes is 2 or 3, and wherein the estimating uses the formula provided on the last line of Table 1 in column 4 or column 5.

21. The method of claim 17, wherein the number of haplotypes is 4 or more, and wherein the estimating uses the formula provided on the last line of Table 1 in column 5.

22. A method for identifying a genetic region associated with a disease, the method comprising:

(a) providing a plurality of single-nucleotide polymorphisms and a plurality of haplotypes for one or more regions of a chromosome;

(b) identifying the number of single-nucleotide polymorphisms of said plurality in at least weak linkage disequilibrium with each other on said chromosomal regions;

(c) comparing the number of single nucleotide polymorphisms in linkage disequilibrium to the number of haplotypes in said chromosomal regions; and

(d) selecting a correlation test, wherein a single-nucleotide-based correlation test is selected if the number of single-nucleotide polymorphisms in linkage disequilibrium is smaller than the number of haplotypes and a number of haplotype-based correlation test is selected if the number of single-nucleotide polymorphisms in linkage disequilibrium is greater than the number of haplotypes, thereby identifying a genetic region associated with a disease.

23. The method of claim 22, wherein the haplotype-based correlation test is a regression test.

24. The method of claim 21, wherein the haplotype-based correlation test is ANOVA test.

25. A method for identifying a genetic region associated with responsiveness to an agent, the method comprising:

(a) providing a plurality of single-nucleotide polymorphisms and a plurality of haplotypes for one or more regions of a chromosome;

(b) identifying the number of single-nucleotide polymorphisms of said plurality in at least weak linkage disequilibrium with each other on said chromosomal regions;

(c) comparing the number of single-nucleotide polymorphisms in linkage disequilibrium to the number of haplotypes in said chromosomal regions; and

(d) selecting a correlation test, wherein a single nucleotide-based correlation test is selected if the number of single-nucleotide polymorphisms in linkage disequilibrium is smaller than the number of haplotypes, thereby identifying a genetic region associated with responsiveness to an agent.

26. The method of claim 25, wherein the haplotype-based correlation test is a regression test.

27. The method of claim 25, wherein the haplotype-based correlation test is ANOVA test.